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 <120> TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL
 LINES
 THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
 IDENTIFICATION OF TASTE COMPOUNDS
 <130> FILE REFERENCE: 078003-0291566
 <140> CURRENT APPLICATION NUMBER:10725076
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 <150> PRIOR APPLICATION NUMBER: US/10/179,373
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 <150> PRIOR APPLICATION NUMBER: 60/304,749
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 <150> PRIOR APPLICATION NUMBER: 60/310,493
 <151> PRIOR FILING DATE: 2001-08-08
 <150> PRIOR APPLICATION NUMBER: 60/331,771
 <151> PRIOR FILING DATE: 2001-11-21
 <150> PRIOR APPLICATION NUMBER: 60/339,472
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 <150> PRIOR APPLICATION NUMBER: 60/372,090
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 <151> PRIOR FILING DATE: 2002-04-22
 <160> NUMBER OF SEQ ID NOS: 19
 <170> SOFTWARE: PatentIn Ver. 2.1
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 <211> LENGTH: 5
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 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: PDZIP
 sequence
 <400> SEQUENCE: 1
 Ser Val Ser Thr Trp
 1 5
 <210> SEQ ID NO 2
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 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
 sequence
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 <221> NAME/KEY: MOD_RES
 <222> LOCATION: (1)
 <223> OTHER INFORMATION: Thr or Arg
 <220> FEATURE:
 <221> NAME/KEY: MOD_RES

<222> LOCATION: (3)
 <223> OTHER INFORMATION: Phe or Leu
 <220> FEATURE:
 <221> NAME/KEY: MOD_RES
 <222> LOCATION: (4)
 <223> OTHER INFORMATION: Arg, Gln or Pro
 <220> FEATURE:
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 <223> OTHER INFORMATION: Arg or Thr
 <220> FEATURE:
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 <222> LOCATION: (7)
 <223> OTHER INFORMATION: Ser, Pro or Val
 <220> FEATURE:
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 <222> LOCATION: (8)
 <223> OTHER INFORMATION: Val, Glu, Arg, Lys or Thr
 <220> FEATURE:
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 <222> LOCATION: (11)
 <223> OTHER INFORMATION: Ala or Glu
 <220> FEATURE:
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 <222> LOCATION: (12)
 <223> OTHER INFORMATION: Trp or Leu
 <220> FEATURE:
 <221> NAME/KEY: MOD_RES
 <222> LOCATION: (13)
 <223> OTHER INFORMATION: Arg, His or Gly
 <400> SEQUENCE: 2
 Xaa Cys Xaa Xaa Arg Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Glu
 1 5 10

<210> SEQ ID NO 3
 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
 sequence
 <220> FEATURE:
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 <222> LOCATION: (1)
 <223> OTHER INFORMATION: Leu or Gln
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 <222> LOCATION: (3)
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 <222> LOCATION: (4)
 <223> OTHER INFORMATION: Asn, Arg or Cys
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<223> OTHER INFORMATION: Arg or Lys
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 <222> LOCATION: (10)
 <223> OTHER INFORMATION: Cys, Gly or Phe
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 <223> OTHER INFORMATION: Val, Leu or Ile
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 <223> OTHER INFORMATION: Ala or Ser
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 <223> OTHER INFORMATION: Met or Leu
 <400> SEQUENCE: 3

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<210> SEQ ID NO 4
 <211> LENGTH: 858
 <212> TYPE: PRT
 <213> ORGANISM: Rattus sp.
 <400> SEQUENCE: 4

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		20					25						30		
Gly	Asp	Tyr	Ile	Leu	Gly	Gly	Leu	Phe	Pro	Leu	Gly	Thr	Thr	Glu	Glu
		35					40					45			
Ala	Thr	Leu	Asn	Gln	Arg	Thr	Gln	Pro	Asn	Gly	Ile	Leu	Cys	Thr	Arg
	50					55					60				
Phe	Ser	Pro	Leu	Gly	Leu	Phe	Leu	Ala	Met	Ala	Met	Lys	Met	Ala	Val
	65				70					75					80
Glu	Glu	Ile	Asn	Asn	Gly	Ser	Ala	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly
				85					90					95	
Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Thr	Met	Lys	Pro
			100					105					110		
Ser	Leu	Met	Phe	Met	Ala	Lys	Val	Gly	Ser	Gln	Ser	Ile	Ala	Ala	Tyr
		115				120						125			
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro
	130					135					140				
His	Ser	Ser	Glu	Leu	Ala	Leu	Ile	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe
	145				150					155					160
Leu	Met	Pro	Gln	Val	Ser	Tyr	Ser	Ala	Ser	Met	Asp	Arg	Leu	Ser	Asp
				165					170					175	
Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val
			180					185					190		
Gln	Leu	Gln	Ala	Val	Val	Thr	Leu	Gln	Asn	Phe	Ser	Trp	Asn	Trp	
		195					200				205				
Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Tyr	Gly	Arg	Glu	Gly	Leu	Ser	
		210				215				220					
Ile	Phe	Ser	Gly	Leu	Ala	Asn	Ser	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu
					230					235					240

Gly	Leu	Val	Pro	Gln	His	Asp	Thr	Ser	Gly	Gln	Gln	Leu	Gly	Lys	Val	
				245					250					255		
Val	Asp	Val	Leu	Arg	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val	
			260					265					270			
Leu	Phe	Ala	Ser	Ala	Arg	Ala	Val	Tyr	Ser	Leu	Phe	Ser	Tyr	Ser	Ile	
		275					280					285				
Leu	His	Asp	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ser	Trp	Leu	
	290					295					300					
Thr	Ser	Asp	Leu	Val	Met	Thr	Leu	Pro	Asn	Ile	Ala	Arg	Val	Gly	Thr	
305					310					315					320	
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Leu	Leu	Pro	Glu	Phe	Ser	His	
			325					330						335		
Tyr	Val	Glu	Thr	Arg	Leu	Ala	Leu	Ala	Ala	Asp	Pro	Thr	Phe	Cys	Ala	
			340					345					350			
Ser	Leu	Lys	Ala	Glu	Leu	Asp	Leu	Glu	Glu	Arg	Val	Met	Gly	Pro	Arg	
		355					360					365				
Cys	Ser	Gln	Cys	Asp	Tyr	Ile	Met	Leu	Gln	Asn	Leu	Ser	Ser	Gly	Leu	
	370					375					380					
Met	Gln	Asn	Leu	Ser	Ala	Gly	Gln	Leu	His	His	Gln	Ile	Phe	Ala	Thr	
385					390					395					400	
Tyr	Ala	Ala	Val	Tyr	Ser	Val	Ala	Gln	Ala	Leu	His	Asn	Thr	Leu	Gln	
			405					410						415		
Cys	Asn	Val	Ser	His	Cys	His	Thr	Ser	Glu	Pro	Val	Gln	Pro	Trp	Gln	
		420						425					430			
Leu	Leu	Glu	Asn	Met	Tyr	Asn	Met	Ser	Phe	Arg	Ala	Arg	Asp	Leu	Thr	
		435					440					445				
Leu	Gln	Phe	Asp	Ala	Lys	Gly	Ser	Val	Asp	Met	Glu	Tyr	Asp	Leu	Lys	
	450					455					460					
Met	Trp	Val	Trp	Gln	Ser	Pro	Thr	Pro	Val	Leu	His	Thr	Val	Gly	Thr	
465					470					475					480	
Phe	Asn	Gly	Thr	Leu	Gln	Leu	Gln	His	Ser	Lys	Met	Tyr	Trp	Pro	Gly	
			485						490					495		
Asn	Gln	Val	Pro	Val	Ser	Gln	Cys	Ser	Arg	Gln	Cys	Lys	Asp	Gly	Gln	
		500						505					510			
Val	Arg	Arg	Val	Lys	Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp	
		515					520					525				
Cys	Lys	Ala	Gly	Ser	Tyr	Arg	Lys	His	Pro	Asp	Asp	Phe	Thr	Cys	Thr	
	530					535					540					
Pro	Cys	Gly	Lys	Asp	Gln	Trp	Ser	Pro	Glu	Lys	Ser	Thr	Thr	Cys	Leu	
545					550					555					560	
Pro	Arg	Arg	Pro	Lys	Phe	Leu	Ala	Trp	Gly	Glu	Pro	Ala	Val	Leu	Ser	
			565						570					575		
Leu	Leu	Leu	Leu	Leu	Cys	Leu	Val	Leu	Gly	Leu	Thr	Leu	Ala	Ala	Leu	
			580					585					590			
Gly	Leu	Phe	Val	His	Tyr	Trp	Asp	Ser	Pro	Leu	Val	Gln	Ala	Ser	Gly	
		595					600					605				
Gly	Ser	Leu	Phe	Cys	Phe	Gly	Leu	Ile	Cys	Leu	Gly	Leu	Phe	Cys	Leu	
	610					615					620					
Ser	Val	Leu	Leu	Phe	Pro	Gly	Arg	Pro	Arg	Ser	Ala	Ser	Cys	Leu	Ala	
625					630					635					640	
Gln	Gln	Pro	Met	Ala	His	Leu	Pro	Leu	Thr	Gly	Cys	Leu	Ser	Thr	Leu	
			645						650					655		
Phe	Leu	Gln	Ala	Ala	Glu	Ile	Phe	Val	Glu	Ser	Glu	Leu	Pro	Leu	Ser	
		660						665					670			
Trp	Ala	Asn	Trp	Leu	Cys	Ser	Tyr	Leu	Arg	Gly	Pro	Trp	Ala	Trp	Leu	
		675					680					685				
Val	Val	Leu	Leu	Ala	Thr	Leu	Val	Glu	Ala	Ala	Leu	Cys	Ala	Trp	Tyr	
	690					695					700					
Leu	Met	Ala	Phe	Pro	Pro	Glu	Val	Val	Thr	Asp	Trp	Gln	Val	Leu	Pro	
705					710					715					720	

Thr	Glu	Val	Leu	Glu	His	Cys	Arg	Met	Arg	Ser	Trp	Val	Ser	Leu	Gly	
				725					730					735		
Leu	Val	His	Ile	Thr	Asn	Ala	Val	Leu	Ala	Phe	Leu	Cys	Phe	Leu	Gly	
			740					745					750			
Thr	Phe	Leu	Val	Gln	Ser	Gln	Pro	Gly	Arg	Tyr	Asn	Arg	Ala	Arg	Gly	
		755					760					765				
Leu	Thr	Phe	Ala	Met	Leu	Ala	Tyr	Phe	Ile	Ile	Trp	Val	Ser	Phe	Val	
	770					775					780					
Pro	Leu	Leu	Ala	Asn	Val	Gln	Val	Ala	Tyr	Gln	Pro	Ala	Val	Gln	Met	
785					790					795					800	
Gly	Ala	Ile	Leu	Phe	Cys	Ala	Leu	Gly	Ile	Leu	Ala	Thr	Phe	His	Leu	
				805					810					815		
Pro	Lys	Cys	Tyr	Val	Leu	Leu	Trp	Leu	Pro	Glu	Leu	Asn	Thr	Gln	Glu	
			820					825					830			
Phe	Phe	Leu	Gly	Arg	Ser	Pro	Lys	Glu	Ala	Ser	Asp	Gly	Asn	Ser	Gly	
		835					840					845				
Ser	Ser	Glu	Ala	Thr	Arg	Gly	His	Ser	Glu							
	850					855										

<210> SEQ ID NO 5

<211> LENGTH: 841

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

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Cys	Cys	Trp	Ala	Phe	Ala	Cys	His	Ser	Thr	Glu	Ser	Ser	Pro	Asp	Phe	
			20					25					30			
Thr	Leu	Pro	Gly	Asp	Tyr	Leu	Leu	Ala	Gly	Leu	Phe	Pro	Leu	His	Ser	
		35				40						45				
Gly	Cys	Leu	Gln	Val	Arg	His	Arg	Pro	Glu	Val	Thr	Leu	Cys	Asp	Arg	
	50				55						60					
Ser	Cys	Ser	Phe	Asn	Glu	His	Gly	Tyr	His	Leu	Phe	Gln	Ala	Met	Arg	
65				70					75					80		
Leu	Gly	Val	Glu	Glu	Ile	Asn	Asn	Ser	Thr	Ala	Leu	Leu	Pro	Asn	Ile	
			85						90					95		
Thr	Leu	Gly	Tyr	Gln	Leu	Tyr	Asp	Val	Cys	Ser	Asp	Ser	Ala	Asn	Val	
			100					105					110			
Tyr	Ala	Thr	Leu	Arg	Val	Leu	Ser	Leu	Pro	Gly	Gln	His	His	Ile	Glu	
		115				120						125				
Leu	Gln	Gly	Asp	Leu	Leu	His	Tyr	Ser	Pro	Thr	Val	Leu	Ala	Val	Ile	
	130					135					140					
Gly	Pro	Asp	Ser	Thr	Asn	Arg	Ala	Ala	Thr	Thr	Ala	Ala	Leu	Leu	Ser	
145				150					155					160		
Pro	Phe	Leu	Val	Pro	Met	Ile	Ser	Tyr	Ala	Ala	Ser	Ser	Glu	Thr	Leu	
			165					170						175		
Ser	Val	Lys	Arg	Gln	Tyr	Pro	Ser	Phe	Leu	Arg	Thr	Ile	Pro	Asn	Asp	
			180					185					190			
Lys	Tyr	Gln	Val	Glu	Thr	Met	Val	Leu	Leu	Leu	Gln	Lys	Phe	Gly	Trp	
		195				200						205				
Thr	Trp	Ile	Ser	Leu	Val	Gly	Ser	Ser	Asp	Asp	Tyr	Gly	Gln	Leu	Gly	
	210					215					220					
Val	Gln	Ala	Leu	Glu	Asn	Gln	Ala	Thr	Gly	Gln	Gly	Ile	Cys	Ile	Ala	
225					230					235				240		
Phe	Lys	Asp	Ile	Met	Pro	Phe	Ser	Ala	Gln	Val	Gly	Asp	Glu	Arg	Met	
			245						250					255		
Gln	Cys	Leu	Met	Arg	His	Leu	Ala	Gln	Ala	Gly	Ala	Thr	Val	Val	Val	
			260					265					270			
Val	Phe	Ser	Ser	Arg	Gln	Leu	Ala	Arg	Val	Phe	Phe	Glu	Ser	Val	Val	
		275					280					285				